

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wahl, Geoffrey M
O'Gorman, Stephen V
- (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 - (B) STREET: 444 South Flower Street, Suite 2000
 - (C) CITY: Los Angeles
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/484,324
 - (B) FILING DATE: 07-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Reiter, Stephen E
 - (B) REGISTRATION NUMBER: 31,192
 - (C) REFERENCE/DOCKET NUMBER: P41 9984
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 546-4737
 - (B) TELEFAX: (619) 546-9392

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: NATIVE FLP
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1269
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT
 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
 1 5 10 15

CGT	CAG	TTT	GTG	GAA	AGG	TTT	GAA	AGA	CCT	TCA	GGT	GAG	AAA	ATA	GCA	96
Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys	Ile	Ala	
			20					25					30			
TTA	TGT	GCT	GCT	GAA	CTA	ACC	TAT	TTA	TGT	TGG	ATG	ATT	ACA	CAT	AAC	144
Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile	Thr	His	Asn	
		35					40					45				
GGA	ACA	GCA	ATC	AAG	AGA	GCC	ACA	TTC	ATG	AGC	TAT	AAT	ACT	ATC	ATA	192
Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr	Asn	Thr	Ile	Ile	
	50					55					60					
AGC	AAT	TCG	CTG	AGT	TTC	GAT	ATT	GTC	AAT	AAA	TCA	CTC	CAG	TTT	AAA	240
Ser	Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn	Lys	Ser	Leu	Gln	Phe	Lys	
65					70					75					80	
TAC	AAG	ACG	CAA	AAA	GCA	ACA	ATT	CTG	GAA	GCC	TCA	TTA	AAG	AAA	TTG	288
Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu	Ala	Ser	Leu	Lys	Lys	Leu	
				85					90					95		
ATT	CCT	GCT	TGG	GAA	TTT	ACA	ATT	ATT	CCT	TAC	TAT	GGA	CAA	AAA	CAT	336
Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile	Pro	Tyr	Tyr	Gly	Gln	Lys	His	
			100					105					110			
CAA	TCT	GAT	ATC	ACT	GAT	ATT	GTA	AGT	AGT	TTG	CAA	TTA	CAG	TTC	GAA	384
Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val	Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	
		115					120					125				
TCA	TCG	GAA	GAA	GCA	GAT	AAG	GGA	AAT	AGC	CAC	AGT	AAA	AAA	ATG	CTT	432
Ser	Ser	Glu	Glu	Ala	Asp	Lys	Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	
	130					135					140					
AAA	GCA	CTT	CTA	AGT	GAG	GGT	GAA	AGC	ATC	TGG	GAG	ATC	ACT	GAG	AAA	480
Lys	Ala	Leu	Leu	Ser	Glu	Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	
145					150					155					160	
ATA	CTA	AAT	TCG	TTT	GAG	TAT	ACT	TCG	AGA	TTT	ACA	AAA	ACA	AAA	ACT	528
Ile	Leu	Asn	Ser	Phe	Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	
				165					170					175		
TTA	TAC	CAA	TTC	CTC	TTC	CTA	GCT	ACT	TTC	ATC	AAT	TGT	GGA	AGA	TTC	576
Leu	Tyr	Gln	Phe	Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	
			180					185					190			
AGC	GAT	ATT	AAG	AAC	GTT	GAT	CCG	AAA	TCA	TTT	AAA	TTA	GTC	CAA	AAT	624
Ser	Asp	Ile	Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	
		195					200					205				
AAG	TAT	CTG	GGA	GTA	ATA	ATC	CAG	TGT	TTA	GTG	ACA	GAG	ACA	AAG	ACA	672
Lys	Tyr	Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr	
	210					215				220						
AGC	GTT	AGT	AGG	CAC	ATA	TAC	TTC	TTT	AGC	GCA	AGG	GGT	AGG	ATC	GAT	720
Ser	Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp	
225					230					235					240	
CCA	CTT	GTA	TAT	TTG	GAT	GAA	TTT	TTG	AGG	AAT	TCT	GAA	CCA	GTC	CTA	768
Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val	Leu	
				245					250					255		
AAA	CGA	GTA	AAT	AGG	ACC	GGC	AAT	TCT	TCA	AGC	AAT	AAA	CAG	GAA	TAC	816
Lys	Arg	Val	Asn	Arg	Thr	Gly	Asn	Ser	Ser	Ser	Asn	Lys	Gln	Glu	Tyr	
			260				265						270			
CAA	TTA	TTA	AAA	GAT	AAC	TTA	GTC	AGA	TCG	TAC	AAT	AAA	GCT	TTG	AAG	864
Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys	Ala	Leu	Lys	
		275					280					285				

100554.0500

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 423 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu	Val
1				5					10					15	
Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys	Ile	Ala
			20					25					30		
Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile	Thr	His	Asn
		35					40					45			
Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr	Asn	Thr	Ile	Ile
	50					55					60				
Ser	Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn	Lys	Ser	Leu	Gln	Phe	Lys
65					70					75					80

Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
 85 90 95
 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
 100 105 110
 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
 115 120 125
 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
 130 135 140
 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
 145 150 155 160
 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
 165 170 175
 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
 180 185 190
 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
 195 200 205
 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
 210 215 220
 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
 225 230 235 240
 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
 245 250 255
 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
 260 265 270
 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
 275 280 285
 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
 290 295 300
 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
 305 310 315 320
 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
 325 330 335
 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
 340 345 350
 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
 355 360 365
 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
 370 375 380
 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
 385 390 395 400
 Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
 405 410 415
 Ser Tyr Ile Asn Arg Arg Ile
 420

10036542.022802

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

34

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG

60

GAACTTCA

68

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